

DNA SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2003, 18:45:51 ; Search time 7198 Seconds
(without alignments)
11219.172 Million cell updates/sec

Title: US-08-785-455-1
Perfect score: 1974
Sequence: 1 ATGGCTAAAGAAACATTTTA.....ATGGTGCAGTGATTAAATAA 1974

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
	1	1974	100.0	1974	6	A64012	A64012 Sequence 1
	2	1974	100.0	1974	6	A79563	A79563 Sequence 1
	3	1974	100.0	301050	1	AP003130	AP003130 Staphyloc
	4	1974	100.0	343590	1	AP003359	AP003359 Staphyloc
	5	1964.4	99.5	1974	6	AX741792	AX741792 Sequence
	6	1961.4	99.4	1971	6	AX619396	AX619396 Sequence
	7	1961.2	99.4	325350	1	AP004823	AP004823 Staphyloc
	8	1959.6	99.3	1974	6	AX741794	AX741794 Sequence
c	9	1350.6	68.4	3500	1	AF270118	AF270118 Staphyloc
c	10	1350.6	68.4	3500	6	AX145436	AX145436 Sequence
c	11	1350.6	68.4	300275	1	AE016751	AE016751 Staphyloc
	12	1267	64.2	1857	6	AX142137	AX142137 Sequence
	13	970.4	49.2	290029	1	AE017024	AE017024 Bacillus
	14	965.6	48.9	307343	1	AE016998	AE016998 Bacillus
c	15	928.4	47.0	3737	1	AF269480	AF269480 Staphyloc
c	16	928.4	47.0	3737	6	AX144800	AX144800 Sequence
	17	865.8	43.9	231450	1	AL596163	AL596163 Listeria
	18	865.8	43.9	349980	6	AX415067	AX415067 Sequence
	19	865.8	43.9	349980	6	AX453571	AX453571 Sequence
	20	853.6	43.2	200050	1	AL591973	AL591973 Listeria
	21	853.6	43.2	349980	6	AX638811	AX638811 Sequence
	22	844	42.8	4340	6	AX416751	AX416751 Sequence
	23	808.6	41.0	300050	1	AP004593	AP004593 Oceanobac
	24	785	39.8	180136	1	BAC180K	D26185 B. subtilis
	25	785	39.8	213080	1	BSUB0001	Z99104 Bacillus su
	26	749.8	38.0	300225	1	AE016949	AE016949 Enterococ
	27	724.6	36.7	300150	1	AP001507	AP001507 Bacillus
	28	716.2	36.3	1998	6	AX608184	AX608184 Sequence
c	29	716.2	36.3	22261	1	AE014263	AE014263 Streptoco
	30	716.2	36.3	82523	6	AX602205	AX602205 Sequence
c	31	716.2	36.3	174050	1	SAG766852	AL766852 Streptoco
	32	681	34.5	10348	1	AE006312	AE006312 Lactococc
c	33	647.2	32.8	323930	1	AP003194	AP003194 Clostridi

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OM nucleic - nucleic search, using sw model

```
Run on:      October 7, 2003, 18:05:31 ; Search time 538 Seconds
              (without alignments)
              9904.630 Million cell updates/sec
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Title: US-08-785-455-1
Perfect score: 1974
Sequence: 1 ATGGCTAAAGAAACATTTTA.....ATGGTGCAGTGATTAAATAA 1974

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query			DB	ID	Description
No.	Score	Match	Length					
1	1974	100.0	1974	18	AAT71309			DNA encoding methi
2	1964.4	99.5	1974	23	AAS55278			Staphylococcus aur
3	1938.8	98.2	1974	23	AAS54400			Staphylococcus aur
4	1927.2	97.6	1960	23	AAS52259			Staphylococcus aur
5	1889.8	95.7	10322	18	AAV74409			Staphylococcus aur
6	1350.6	68.4	1983	24	ABN91050			Staphylococcus epi
c 7	1350.6	68.4	3500	22	AAH54794			S. epidermidis gen
8	1267	64.2	1857	22	AAH52733			S. epidermidis ope
9	1162	58.9	1170	23	AAS55386			Staphylococcus aur
c 10	928.4	47.0	3737	22	AAH54158			S. epidermidis gen
11	865.8	43.9	1163020	24	ABQ67197			Listeria innocua c
12	865.8	43.9	3011208	24	ABQ69245			Listeria innocua D
13	853.6	43.2	2944528	24	ABA03041			Listeria monocytog
14	844	42.8	4340	24	ABQ70929			Listeria monocytog
15	749.8	38.0	2034	23	AAS52929			Enterococcus faeca
16	748.8	37.9	9589	20	AAX13193			Enterococcus faeca
17	748.8	37.9	9589	24	ABS98988			Enterococcus faeca
18	747	37.8	1998	23	AAS51296			Enterococcus faeca
c 19	716.2	36.3	2155561	24	ABN71527			Streptococcus poly
20	715	36.2	1995	24	ABN71065			Streptococcus poly
21	715	36.2	2046	24	ABN67156			Streptococcus poly
22	681	34.5	2365589	24	ABA90521			Genomic sequence o
c 23	672.6	34.1	703	23	AAS50259			Staphylococcus aur
24	623	31.6	2040	23	AAS55683			Streptococcus pneu
25	623	31.6	2162598	25	ABS56454			Streptococcus pneu
c 26	622.6	31.5	10690	19	AAV52226			Streptococcus pneu
27	621.8	31.5	1995	25	ABX06461			S. pneumoniae type
28	612.4	31.0	1998	18	AAT88098			Streptococcus pneu
c 29	591.6	30.0	4392	19	AAZ96285			S. pneumoniae deri
c 30	591.6	30.0	4392	19	AAV37375			Streptococcus pneu
31	532	27.0	1998	24	ABN67157			Streptococcus poly
c 32	516.8	26.2	520	23	AAS49691			Staphylococcus aur
c 33	515.4	26.1	517	23	AAS49996			Staphylococcus aur
c 34	465.8	23.6	520	23	AAS49750			Staphylococcus aur
c 35	465.8	23.6	520	23	AAS49785			Staphylococcus aur
c 36	465.8	23.6	520	23	AAS50541			Staphylococcus aur
c 37	359.4	18.2	361	23	AAS49732			Staphylococcus aur
c 38	359.4	18.2	361	23	AAS49739			Staphylococcus aur
c 39	359.4	18.2	361	23	AAS50731			Staphylococcus aur
40	316.2	16.0	3029	22	AAH54833			S. epidermidis gen
41	315	16.0	531	22	AAH53469			S. epidermidis ope
42	294.6	14.9	3478	22	AAH54241			S. epidermidis gen
43	265.8	13.5	756	24	ABK73919			Bacillus lichenifo
44	257.6	13.0	2157	19	AAV53135			Helicobacter methi
45	253.6	12.8	1971	23	AAS53820			Helicobacter pylor

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

11436.719 Million cell updates/sec

Sequence: 1 ATGGCTAAAGAAACATTTTA.....ATGGTGCAGTGATTAAATAA 1974

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Maximum DB seq length: 2000000000

Listing first 45 summaries

```

1:  em_estba:*
2:  em_esthum:*
3:  em_estin:*
4:  em_estmu:*
5:  em_estov:*
6:  em_estpl:*
7:  em_estro:*
8:  em_htc:*
9:  gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*

```

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	202	10.2	454	9	AI759279	AI759279 EtESTeal5
	2	148.4	7.5	574	12	BM275799	BM275799 PfESToaa8
	3	144.6	7.3	872	14	CD376435	CD376435 PTMM01602
	4	132.6	6.7	651	28	BH003849	BH003849 BMBAC07A1
	5	126	6.4	673	28	BH242417	BH242417 ATZFD11TF
	6	122	6.2	800	12	BI931841	BI931841 EST551730
	7	113.6	5.8	656	13	BW210661	BW210661 BW210661
c	8	112.8	5.7	3515	11	BC050225	BC050225 Mus muscu
	9	109.8	5.6	501	10	BE587843	BE587843 WHE0670_F
	10	109	5.5	641	9	AV969896	AV969896 AV969896
	11	105	5.3	554	13	BU496455	BU496455 PfESToab5
	12	104.2	5.3	1902	11	AK050196	AK050196 Mus muscu
	13	104.2	5.3	2812	11	AK042888	AK042888 Mus muscu
	14	100	5.1	715	10	BG130580	BG130580 EST476322
	15	98.6	5.0	543	14	CA925240	CA925240 MTU7TL.P1
	16	97.6	4.9	753	12	BG889721	BG889721 EST515572
	17	97.2	4.9	582	9	AW774279	AW774279 EST333430
	18	95.6	4.8	966	29	CNS06NX2	AL407340 T7 end of
	19	95	4.8	469	14	CB971564	CB971564 CAB10005
	20	93.2	4.7	596	12	BM813204	BM813204 EST591297
	21	92.6	4.7	689	13	BU001007	BU001007 QGG26K11.
	22	92.6	4.7	841	14	CB623335	CB623335 OSIIEa11A
	23	90.8	4.6	413	13	BQ588356	BQ588356 E012308-0
c	24	90.2	4.6	533	29	TA262E03P	AL484163 T. brucei
	25	88.6	4.5	615	10	BF299086	BF299086 065PbH03
	26	86.6	4.4	667	14	CA839757	CA839757 MCT031A05
	27	86.4	4.4	838	28	BH146733	BH146733 ENTQN84TF
c	28	86	4.4	953	29	CNS06DTD	AL394247 T3 end of
	29	85.4	4.3	474	13	BQ114403	BQ114403 EST599979
	30	85.4	4.3	697	13	BW030664	BW030664 BW030664
	31	83.6	4.2	602	9	AV827139	AV827139 AV827139
	32	82.6	4.2	825	14	CB624415	CB624415 OSIIEa12P
	33	82.4	4.2	819	13	BX076739	BX076739 BX076739
	34	82.2	4.2	576	12	BI814974	BI814974 PfESToaa0
	35	81.4	4.1	577	12	BG889902	BG889902 EST515753
	36	77.2	3.9	843	13	BX074933	BX074933 BX074933
	37	74.4	3.8	580	14	CA839088	CA839088 MCT023F12
	38	73.6	3.7	493	10	BF052373	BF052373 EST437603
c	39	73.4	3.7	508	28	AZ655235	AZ655235 1M0530B09
c	40	73.2	3.7	842	28	AZ675025	AZ675025 ENTHQ03TF
c	41	71.4	3.6	574	29	BZ298881	BZ298881 CG4634.r1
	42	71.2	3.6	404	10	BF052377	BF052377 EST437607
c	43	71.2	3.6	992	28	BH163124	BH163124 ENTQS24TR
c	44	71	3.6	985	29	CNS06NX3	AL407341 T3 end of
	45	70.4	3.6	911	28	AZ540287	AZ540287 ENTGN30TF

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

```
Run on:      October  7, 2003, 22:11:28 ; Search time 493 Seconds
              (without alignments)
              10213.802 Million cell updates/sec
```

Title: US-08-785-455-1
Perfect score: 1974
Sequence: 1 ATGGCTAAAGAAACATTTTA.....ATGGTGCAGTGATTAAATAA 1974

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						
No.	Score	Query Match	Length	DB	ID	Description	
	1	1964.4	99.5	1974	9	US-09-815-242-8915	Sequence 8915, Ap
	2	1948.2	98.7	10322	8	US-08-781-986A-98	Sequence 98, Appl
	3	1938.8	98.2	1974	9	US-09-815-242-8037	Sequence 8037, Ap
	4	1927.2	97.6	1960	9	US-09-815-242-4841	Sequence 4841, Ap
	5	1162	58.9	1170	9	US-09-815-242-9023	Sequence 9023, Ap
	6	749.8	38.0	2034	9	US-09-815-242-6566	Sequence 6566, Ap
	7	748.8	37.9	9589	10	US-09-070-927A-256	Sequence 256, App
	8	747	37.8	1998	9	US-09-815-242-3878	Sequence 3878, Ap
c	9	672.6	34.1	703	9	US-09-815-242-2836	Sequence 2836, Ap
	10	623	31.6	2040	9	US-09-815-242-9320	Sequence 9320, Ap
c	11	516.8	26.2	520	9	US-09-815-242-2268	Sequence 2268, Ap
c	12	515.4	26.1	517	9	US-09-815-242-2573	Sequence 2573, Ap
c	13	465.8	23.6	520	9	US-09-815-242-2327	Sequence 2327, Ap
c	14	465.8	23.6	520	9	US-09-815-242-2362	Sequence 2362, Ap
c	15	465.8	23.6	520	9	US-09-815-242-3118	Sequence 3118, Ap
c	16	359.4	18.2	361	9	US-09-815-242-2309	Sequence 2309, Ap
c	17	359.4	18.2	361	9	US-09-815-242-2316	Sequence 2316, Ap
c	18	359.4	18.2	361	9	US-09-815-242-3308	Sequence 3308, Ap
	19	265.8	13.5	756	10	US-09-974-300-1210	Sequence 1210, Ap
	20	253.6	12.8	1971	9	US-09-815-242-7457	Sequence 7457, Ap
	21	240.6	12.2	536	10	US-09-974-300-1269	Sequence 1269, Ap
c	22	232.4	11.8	234	9	US-09-815-242-1746	Sequence 1746, Ap
c	23	232.4	11.8	234	9	US-09-815-242-1989	Sequence 1989, Ap
	24	211.4	10.7	38459	12	US-09-960-858-3	Sequence 3, Appli
	25	211.4	10.7	38459	12	US-09-960-870-3	Sequence 3, Appli
	26	211.4	10.7	580073	12	US-10-205-220-1	Sequence 1, Appli
	27	183.4	9.3	1851	10	US-09-938-842A-981	Sequence 981, App
c	28	149.2	7.6	45191	15	US-10-080-170-649	Sequence 649, App
	29	147.8	7.5	1734	12	US-10-032-585-6843	Sequence 6843, Ap
	30	127.2	6.4	273	10	US-09-974-300-5686	Sequence 5686, Ap
c	31	98.4	5.0	100	9	US-09-815-242-3582	Sequence 3582, Ap
	32	91.6	4.6	549	10	US-09-974-300-5697	Sequence 5697, Ap
	33	90.6	4.6	261	10	US-09-974-300-2608	Sequence 2608, Ap
	34	80.2	4.1	640681	10	US-09-790-988-1	Sequence 1, Appli
	35	70.6	3.6	446	9	US-09-770-444-777	Sequence 777, App
c	36	67.2	3.4	1830121	14	US-10-329-960-1	Sequence 1, Appli
	37	66.6	3.4	2049	9	US-09-815-242-7117	Sequence 7117, Ap
	38	59.2	3.0	2409	9	US-09-815-242-4542	Sequence 4542, Ap
	39	59.2	3.0	2418	9	US-09-815-242-8188	Sequence 8188, Ap
	40	57.4	2.9	1830	10	US-09-738-626-995	Sequence 995, App
	41	57.4	2.9	3309400	10	US-09-738-626-1	Sequence 1, Appli
c	42	56.2	2.8	363	9	US-09-815-242-2718	Sequence 2718, Ap
c	43	56.2	2.8	363	9	US-09-815-242-2960	Sequence 2960, Ap
	44	56.2	2.8	2034	9	US-09-815-242-6113	Sequence 6113, Ap
	45	56.2	2.8	6501	9	US-09-767-515-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-815-242-8915

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2003, 19:56:17 ; Search time 124 Seconds
(without alignments)
7026.535 Million cell updates/sec

Title: US-08-785-455-1
Perfect score: 1974
Sequence: 1 ATGGCTAAAGAAACATTTTA.....ATGGTGCAGTGATTAAATAA 1974

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	1350.6	68.4	1983	4	US-09-134-001C-513			Sequence 513, App
	2	712	36.1	2025	4	US-09-107-532A-2547			Sequence 2547, Ap
	3	622.6	31.5	10690	4	US-08-961-527-93			Sequence 93, Appl
	4	612.4	31.0	1998	3	US-08-844-059-1			Sequence 1, Appli
	5	612.4	31.0	1998	3	US-09-431-202-1			Sequence 1, Appli
	6	257.6	13.0	2157	1	US-08-451-715A-3			Sequence 3, Appli
	7	247.4	12.5	912	4	US-08-858-207A-202			Sequence 202, App
	8	211.4	10.7	580073	4	US-08-545-528D-1			Sequence 1, Appli
c	9	150.8	7.6	4403765	3	US-09-103-840A-2			Sequence 2, Appli
	10	149.2	7.6	2290	1	US-08-584-226-1			Sequence 1, Appli
c	11	149.2	7.6	4411529	3	US-09-103-840A-1			Sequence 1, Appli
c	12	123.8	6.3	1664976	4	US-08-916-421B-1			Sequence 1, Appli